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A new rock-dwelling gecko of the subgenus *Japonigekko* (Squamata, Gekkonidae, *Gekko*) from northwestern Sichuan Province, China

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Abstract

We describe a new rock-dwelling species of the genus *Gekko* (subgenus *Japonigekko*) from Heishui County, Aba Tibetan and Qiang Autonomous Prefecture, Sichuan Province, China, based on both morphological and molecular (1,574 bp from the mitochondrial 16S rRNA and ND2 genes) evidence. Morphologically, *Gekko tesselatus* **sp. nov.** is characterized by its moderate body size; two (rarely one) enlarged postmentals; flattened dorsal tubercles extending from the posterior head through the neck to the anterior portion of the tail, arranged in 12–15 rows at midbody; 130–157 ventral scales between the mental and the cloacal slit; 98–106 midbody scale rows; 31–39 ventral scale rows; subdigital lamellae numbering 7–10 on finger I, 9–12 on finger IV, 7–9 on toe I, and 9–12 on toe IV; absence of webbing; 6–8 precloacal pores in males and absence in females; one (rarely two) postcloacal tubercle on each side; and a distinctive dorsal coloration. Phylogenetically, the new species forms a distinct clade within the subgenus *Japonigekko*, showing uncorrected 16S sequence divergences of at least 8.2% from its closest relative, *G. liboensis*, and at least 8.9% from all other congeners, as well as ND2 divergences of at least 14.3% from *G. fengshanensis* and at least 14.9% from other species in the subgenus. The discovery of this new species raises the number of *Japonigekko* species recorded in China to 26 and in Sichuan Province to seven.

Key Words

Gekko tesselatus sp. nov., molecular phylogeny, morphological characters, taxonomy

Introduction

The genus *Gekko* Laurenti, 1768, represents a taxonomically diverse group within the family Gekkonidae Gray, 1825. Currently, 93 valid species are recognized within the genus, and its members are widely distributed across eastern and southeastern Asia, as well as parts of northwestern Oceania and Melanesia (Ma et al. 2024; Cao et al. 2025; Huang et al. 2025; Pauwels et al. 2025; Uetz et al. 2025). Due to the high morphological similarity among species, which complicates diagnosis and hampers the identification of cryptic lineages, the taxonomy of the genus *Gekko* remained unre-

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solved for long period of time (Zhao and Adler 1993; Zhao et al. 1999; Kluge 1993, 2001; Rösler et al. 2005, 2011). In recent years, however, the use of integrative taxonomic approaches that combine detailed morphological assessments with molecular phylogenetic analyses has clarified many previously ambiguous species boundaries and gradually revealed the true extent of diversity within the genus (Brown et al. 2009; Rösler et al. 2011; Luu et al. 2015; Wood et al. 2020; Lyu et al. 2021; Xia et al. 2023; Huang et al. 2025).

According to the classification proposed by Wood et al. (2020), the genus is currently divided into seven subgenera: *Gekko* s. str., *Japonigekko* Wood, Guo, Travers, Su, Olson, Bauer, Grismer, Siler, Moyle, Andersen & Brown, *Ptychozoon* Kuhl & Van Hasselt, *Rhacogekko* Wood, Guo, Travers, Su, Olson, Bauer, Grismer, Siler, Moyle, Andersen & Brown, *Lomatodactylus* van der Hoeven, *Balawangekko* Wood, Guo, Travers, Su, Olson, Bauer, Grismer, Siler, Moyle, Andersen & Brown, and *Archipelagekko* Wood, Guo, Travers, Su, Olson, Bauer, Grismer, Siler, Moyle, Andersen & Brown. Among these, *Japonigekko* is the most diverse group, comprising 38 species, 25 of which occur in China (Cao et al. 2025; Huang et al. 2025; Zhou et al. 2025b). Members of *Japonigekko* are characterized by the following diagnostic features: moderate body size; nares usually in contact with the rostral; 2–4 nasals (including nasorostrals, supranasals, and postnasals); 0–21 rows of dorsal tubercles; 0–32 precloacal pores; 1–4 postcloacal tubercles; and lateral folds lacking tubercles (Wood et al. 2020; Hou et al. 2021; Ma et al. 2024; Wang et al. 2024; Zhou et al. 2025a; Uetz et al. 2025).

Located in western China, Sichuan Province encompasses several major geomorphological regions, including the Qinghai–Xizang Plateau, the Hengduan Mountains, the Yunnan–Guizhou Plateau, the Qinba Mountains, and the Sichuan Basin. Its complex geological structure and highly diverse topography have given rise to a complex and varied climate. Together with significant geographical barriers and a mosaic of microhabitats, these conditions have driven pronounced regional differentiation of species. Consequently, Sichuan supports exceptionally high levels of biodiversity and is recognized as one of China's most important reservoirs of genetic resources. During a field survey conducted in the summer of 2025, we collected a series of *Gekko* (*Japonigekko*) specimens from a dry-hot valley in Heishui County, Aba Tibetan and Qiang Autonomous Prefecture, Sichuan Province, China (Fig. 1). However, detailed morphological comparisons and mitochondrial DNA analyses revealed that these individuals differ markedly from all known *Gekko* species. Based on this evidence, we herein describe this population as a new species.

Material and methods

Sampling

Field surveys were conducted in the dry-hot valley of Heishui County, Sichuan Province, China, in the summer of 2025. Geographic coordinates and elevation were recorded using the TwoStep Outdoor Assistant v7.9.13 (Shenzhen 2bulu Information Technology Co., Ltd., Shenzhen, China). After being photographed, all newly collected specimens were humanely euthanized using a lethal injection of 0.7% tricaine methanesulfonate (MS-222) solution, then fixed in 95% ethanol for one day and transferred to 75% ethanol for long-term preservation. Fresh liver tissue was extracted, immediately preserved in 95% ethanol, and stored at –20 °C. The specimens were deposited at Qinghai University (QHU), the Museum of Biology, Sun Yat-sen University (SYS), and the Chengdu Institute of Biology (CIB), Chinese Academy of Sciences. All sampling procedures involving live geckos complied with the Wildlife Protection Law of China and were approved by the Institutional Ethics Committee of Qinghai University (Protocol No. PJ202501-89).

Molecular phylogeny

Since all specimens were collected from the same locality and showed consistent morphological traits, we randomly selected 10 individuals for DNA sequencing. Total genomic DNA was extracted from preserved liver tissue using the QIAamp DNA Mini Kit (QIAGEN, Changsheng Biotechnology Co., Ltd.). Two mitochondrial gene fragments, 16S ribosomal RNA (16S) and NADH dehydrogenase subunit 2 (ND2), were amplified via polymerase chain reaction (PCR) following the protocols outlined by Wang et al. (2024). The following primer pairs were used: L3975 (5'-CGCCTGTTTACCAAAAACAT-3') and H4551 (5'-CCGGTCTGAACTCAGATCACGT-3') for 16S (Simon et al. 1994), and rMet-3L (5'-ATACCCCGACAATGTTGG-3') and rAla-1H (5'-GCCTTAGCTTAATTAAAGTG-3') for ND2 (Jonniaux and Kumazawa 2008). The PCR products were sequenced by Shanghai Map Biotech Co., Ltd. Raw sequences were assembled using SeqMan in the DNASTAR software package (Burland 2000). Newly generated sequences have been submitted to the DDBJ; accession numbers are listed in Table 1.

Apart from the 20 newly obtained sequences, we included 80 additional sequences representing 48 individuals from 28 species of the subgenus *Japonigekko* (Table 1). *Gekko gecko* (Linnaeus, 1758) and *G. reevesii* (Gray, 1831) were selected as outgroups, following the approach of Wang et al. (2024). A concatenated dataset of the two gene fragments (16S + ND2, 1,574 bp in total) was aligned using MUSCLE (Edgar 2004) in MEGA X (Kumar et al. 2018). Uncorrected pairwise distances (*p*-distances) between closely related species were also calculated in MEGA X. The Maximum Likelihood (ML) analysis was conducted in IQ-TREE v1.6.12 (Nguyen et al. 2015), partitioned by gene, with both 16S and ND2 fragments independently selected under the best-fit model GTR+F+I+G4 by ModelFinder (Kalyaanamoorthy et al. 2017) implemented in PhyloSuite v1.2.3 (Zhang et al. 2020), according to the Bayesian Information Criterion (BIC) (Kalyaanamoorthy et al. 2017).

Table 1. NCBI/DDBJ accession numbers, localities, and voucher information for all specimens used in this study. * indicates DDBJ accession number.

No.	Species	Localities	Voucher ID.	16S	ND2	Reference
1	*G. tesselatus* sp. nov.	Heishui, Sichuan, China	CIB 119371	LC899308*	LC899318*	This study
2	*G. tesselatus* sp. nov.	Heishui, Sichuan, China	CIB 119372	LC899309*	LC899319*	This study
3	*G. tesselatus* sp. nov.	Heishui, Sichuan, China	CIB 119373	LC899310*	LC899320*	This study
4	*G. tesselatus* sp. nov.	Heishui, Sichuan, China	CIB 119374	LC899311*	LC899321*	This study
5	*G. tesselatus* sp. nov.	Heishui, Sichuan, China	CIB 119375	LC899312*	LC899322*	This study
6	*G. tesselatus* sp. nov.	Heishui, Sichuan, China	QHU R2025022	LC899313*	LC899323*	This study
7	*G. tesselatus* sp. nov.	Heishui, Sichuan, China	QHU R2025023	LC899314*	LC899324*	This study
8	*G. tesselatus* sp. nov.	Heishui, Sichuan, China	QHU R2025024	LC899315*	LC899325*	This study
9	*G. tesselatus* sp. nov.	Heishui, Sichuan, China	QHU R2025025	LC899316*	LC899326*	This study
10	*G. tesselatus* sp. nov.	Heishui, Sichuan, China	QHU R2025026	LC899317*	LC899327*	This study
11	*G. adleri*	Jingxi, Guangxi, China	SYS r001400	MW451654	OR902178	Lyu et al. (2021); Wang et al. (2024)
12	*G. adleri*	Cao Bang, Vietam	IEBR A.2012.24	KC700623	–	Nguyen et al. (2013)
13	*G. alpinus*	Batang, Sichuan, China	CIB 121663	PQ255983	PQ303501	Ma et al. (2024)
14	*G. alpinus*	Mangkang, Xizang, China	CIB 121656	PQ255976	PQ303494	Ma et al. (2024)
15	*G. auriverrucosus*	Yuncheng, Shanxi, China	NNU Z20050801.004	–	JN019062	Rösler et al. (2011)
16	*G. bonkowskii*	Khammouane, Laos	VFU R.2014.10	–	KT266818	Luu et al. 2015
17	*G. chinensis*	Hong Kong, China	SYS r001211	MW451644	OR902183	Lyu et al. (2021); Wang et al. (2024)
18	*G. chinensis*	Shenzhen, Guangdong, China	SYS r001085	MW451632	OR902184	Lyu et al. (2021); Wang et al. (2024)
19	*G. cib*	Hejiang, Sichuan, China	SYS r001489	MW451655	OR902165	Lyu et al. (2021); Wang et al. (2024)
20	*G. cib*	Emeishan, Sichuan, China	SYS r000708	MW451629	OR902166	Lyu et al. (2021); Wang et al. (2024)
21	*G. fengshanensis*	Fengshan, Guangxi, China	NHMG 240713	PV652773	PV657377	Huang et al. (2025)
22	*G. fengshanensis*	Fengshan, Guangxi, China	NHMG 240714	PV652774	PV657378	Huang et al. (2025)
23	*G. hokouensis*	Wuyishan, Fujian, China	SYS r001290	MW451647	OR902173	Lyu et al. (2021); Wang et al. (2024)
24	*G. hokouensis*	Nanchang, Jiangxi, China	SYS r001311	MW451648	OR902172	Lyu et al. (2021); Wang et al. (2024)
25	*G. ichangensis*	Yichang, Hubei, China	SWU 0011602	PQ587503	–	Cao et al. (2025)
26	*G. ichangensis*	Yichang, Hubei, China	SWU 0011603	PQ587504	–	Cao et al. (2025)
27	*G. japonicus*	Wuyishan, Fujian, China	SYS r000672	MW451628	OR902176	Lyu et al. (2021); Wang et al. (2024)
28	*G. japonicus*	Lushan, Jiangxi, China	SYS r001317	MW451649	OR902177	Lyu et al. (2021); Wang et al. (2024)
29	*G. jinjiangensis*	Deqin, Yunan, China	CIB 5334220088	PQ255987	MT449432	Hou et al. (2021); Ma et al. (2024)
30	*G. jinjiangensis*	Derong, Sichuan, China	CIB 5133380017	–	MT449437	Hou et al. (2021)
31	*G. kaiyai*	Xinxian, Henan, China	AHUXXBH01	OQ780318	–	Zhang et al. (2023)
32	*G. kaiyai*	Shangcheng, Henan, China	AHUJGTBH01	OQ780322	–	Zhang et al. (2023)
33	*G. khunkhamensis*	Khammouane, Laos	VNUF R.2021.23	–	OL416111	Sitthivong et al. (2021)
34	*G. kwangsiensis*	Wuming, Guangxi, China	SYS r001195	MW451642	OR902175	Lyu et al. (2021); Wang et al. (2024)
35	*G. kwangsiensis*	Wuming, Guangxi, China	SYS r001194	MW451641	OR902174	Lyu et al. (2021); Wang et al. (2024)
36	*G. liboensis*	Libo, Guizhou, China	SYS r002876	PV652777	PV657381	Huang et al. (2025)
37	*G. liboensis*	Libo, Guizhou, China	SYS r002877	PV652778	PV657382	Huang et al. (2025)
38	*G. melli*	Dongguan, Guangdong, China	SYS r001742	MW451661	OR902169	Lyu et al. (2021); Wang et al. (2024)
39	*G. melli*	Puning, Guangdong, China	SYS r001702	MW451660	OR902170	Lyu et al. (2021); Wang et al. (2024)
40	*G. nadenensis*	Khammouane, Laos	ZFMK 98741	–	KY421618	Luu et al. (2017)
41	*G. palmatus*	Zhaoqing, Guangdong, China	SYS r002797	OR903156	OR902179	Wang et al. (2024)
42	*G. palmatus*	Napo, Guangxi, China	SYS r001185	MW451637	OR902182	Lyu et al. (2021); Wang et al. (2024)
43	*G. paucituberculatus*	Baise, Guangxi, China	SYS r002806	OR903154	OR902163	Wang et al. (2024)
44	*G. paucituberculatus*	Baise, Guangxi, China	SYS r002806	OR903155	OR902164	Wang et al. (2024)
45	*G. prep*	Changjiang, Hainan, China	HN2024R038	PV368865	PV389916	Zhou et al. (2025a)

No.	Species	Localities	Voucher ID.	16S	ND2	Reference
46	*G. prep*	Changjiang, Hainan, China	HN2024R039	PV368866	PV389915	Zhou et al. (2025a)
47	*G. scientiadventura*	Quang Binh, Vietnam	IEBR A.2014.7	–	KP205392	Luu et al. (2014)
48	*G. sengchanthavongi*	Khammouane, Laos	VFU R2014.14	–	KT266816	Luu et al. (2015)
49	*G. similignum*	Wuzhishan, Hainan, China	SYS r001597	MW451658	OR902185	Lyu et al. (2021); Wang et al. (2024)
50	*G. similignum*	Wuzhishan, Hainan, China	SYS r001598	MW451659	OR902186	Lyu et al. (2021); Wang et al. (2024)
51	*G. scabridus*	Yanbian, Sichuan, China	CIB YN201909199	PQ255992	MT449429	Hou et al. (2021); Ma et al. (2024)
52	*G. scabridus*	Yanbian, Sichuan, China	CIB YN201909200	–	MT449430	Hou et al. (2021)
53	*G. subpalmatus*	Fenghua, Zhejiang, China	SYS r001762	MW451662	OR902167	Lyu et al. (2021); Wang et al. (2024)
54	*G. subpalmatus*	Fenghua, Zhejiang, China	SYS r001767	MW451663	OR902168	Lyu et al. (2021); Wang et al. (2024)
55	*G. swinhonis*	Zunhua, Hebei, China	SYS r001814	MW451666	OR902171	Lyu et al. (2021); Wang et al. (2024)
56	*G. swinhonis*	Zunhua, Hebei, China	SYS r001815	MW451667	–	Lyu et al. (2021)
57	*G. thakhekensis*	Thakhek, Khammouane, Laos	IEBR A.2014.6	–	KP205396	Luu et al. (2014)
58	*G. truongi*	Khanh Hoa, Vietnam	IEBR A.2011.1	–	KP205398	Luu et al. (2014)
Out group						
59	*G. gecko*	Nanning, Guangxi, China	N/A	AY282753	AY282753	Zhou et al. (2006)
60	*G. reevesii*	Mt. Yinping, Guangdong, China	SYS r000796	MW451630	OR902187	Lyu et al. (2021); Wang et al. (2024)

Nodes were regarded as well supported when ultrafast bootstrap values (UFB) ≥ 95% and SH-like approximate likelihood ratio test values (SH-aLRT) ≥ 80% (Stephane et al. 2010; Hoang et al. 2018). The phylogenetic tree was visualized using FigTree v1.4.4 (Rambaut 2018).

Morphological examination

Comparisons with other congeners of the subgenus *Japonigekko* were based on available literature: Stejneger (1907); Zhou et al. (1982); Song (1985); Ota et al. (1995); Zhao et al. (1999); Goris and Maeda (2004); Rösler et al. (2005, 2011); Toda et al. (2008); Zhou and Wang (2008); Phung and Ziegler (2011); Nguyen et al. (2013); Luu et al. (2014, 2015, 2017); Jono et al. (2015); Ngo et al. (2015); Yang (2015); Lin and Yao (2016); Hou et al. (2021); Lyu et al. (2021); Sitthivong et al. (2021); Zhang et al. (2023); Ma et al. (2024); Wang et al. (2024); Cao et al. (2025); Huang et al. (2025); Zhou et al. (2025a, b).

Morphological descriptions followed the methodology outlined in Lyu et al. (2021) and Grismer et al. (2022), with certain abbreviations revised according to the standards set following the abbreviations list in Darko et al. (2022). Three morphometric characters were measured with Deli digital calipers (No. 90150B) to the nearest 0.1 mm: **SVL** = snout–vent length, measured from the tip of the snout to the posterior edge of the vent; **TAL** = tail length, measured from the posterior margin of the vent to the tip of the tail; **AGD** = axilla–groin distance, defined as the distance between the posterior edge of the forelimb insertion and the anterior edge of the hindlimb insertion, with both limbs inserted perpendicularly to the body wall. All other measurements were taken using Mitutoyo digital calipers (CD-15AX) to the nearest 0.01 mm under a Leica stereomicroscope (EZ4): **HL** = head length, measured from the tip of the snout to the posterior margin of the ear opening; **HW** = head width, measured at the angle of the jaws; **HH** = head height, measured from the top of the head posterior to the eyes to the bottom of the lower jaw; **ESD** = eye-to-snout distance/snouth length, measured from the tip of the snout to the anterior corner of the eye; **ED** = eye diameter, measured as the greatest distance from the anterior to the posterior corner of the eye; **EL** = maximum ear opening diameter; **RW** = maximum rostral width; **RH** = maximum rostral height; **MW** = maximum mental width; and **ML** = maximum mental length.

Scalation features and their abbreviations were as follows: **NS** = number of nasals, including nasorostrals, supranasals, and postnasals; **INS** = internasals, number of scales between supranasals, in contact with the rostral; **SL** = supralabials; **IL** = infralabials; **IOS** = interorbitals, number of scales in a line between the anterior corners of the eyes; **PO** = preorbitals, number of scales in a line from the nostril to the anterior margin of the eye; **PM** = postmentals, number of scales bordering the mental; **GP** = gulars bordering the postmentals; **MBSR** = midbody scale rows; **VS** = ventral scale rows at midbody; **SMC** = scales in a line from the mental to the front of the cloacal slit; **DTR** = dorsal tubercle rows at midbody; **GSDT** = granules surrounding dorsal tubercles, counted by randomly selecting 10 tubercles on the trunk and recording the number of granules surrounding each; **LF1** = number of the subdigital lamellae beneath the entire first finger; **LF4** = number of the subdigital lamellae beneath the entire fourth finger; **LT1** = number of the subdigital lamellae beneath the entire first toe; **LT4** = number of the subdigital lamellae beneath the entire fourth toe; **PP** = number of the precloacal pores; **PAT** = number of the postcloacal tubercles.

In addition, we recorded the presence or absence of webbing (**Web**); the presence of tubercles on the forelimbs (**Fore tubercles**), hindlimbs (**Hind tubercles**), and tail (**Tail tubercles**); the presence of enlarged subcaudal scales; and the types of dorsal coloration patterns.

Other abbreviations are as follows: **Is.**: Island; **Mt.**: Mountain; **Mts.**: Mountains; **NP**: National Park; **NR**: Nature Reserve; **WS**: Wildlife Sanctuary; **asl.**: above sea level.

Results

The lengths of the 16S and ND2 fragments in the final alignment comprised 563 base pairs (bp) and 1,011 bp, respectively. In the ML analysis (Fig. 2), all *Gekko* (*Japonigekko*) samples included in this study formed a strongly supported monophyletic lineage (SH = 100 / UFB = 100). However, relationships among species within the subgenus remain incompletely resolved due to low nodal support at interspecific levels. The newly collected specimens from Heishui County, Sichuan Province, China, constituted a well-supported monophyletic lineage within *Japonigekko* (SH = 100 / UFB = 100), which was recovered as sister to a clade comprising *G. fengshanensis* Huang, Wang, Qi, Song, Huang, Wang & Mo, 2025, *G. liboensis* Zhou, Liu & Li, 1982, and *G. kwangsiensis* Yang, 2015, although with relatively low support (SH = 80 / UFB = 65). Finally, these four taxa, along with *G. paucituberculatus* Wang, Qi, Zhou & Wang, 2024, formed a well-supported clade (SH = 100 / UFB = 100), whose members exhibit specialized ecological adaptations to rocky environments.

Uncorrected *p*-distances for the 16S and ND2 gene fragments are summarized in Tables 2 and 3, respectively. Interspecific genetic distances within *Japonigekko* ranged from 3.5% between *G. chinensis* (Gray, 1842) and *G. similignum* Smith, 1923 to 16.8% between *G. adleri* Nguyen, Wang, Yang, Lehmann, Le, Ziegler & Bonkowski, 2013 and *G. swinhonis* Günther, 1864 for the 16S gene (Table 2); and from 5.4% between *G. chinensis* and *G. similignum* to 26.7% between *G. prep* Zhou, Chen, Liu, Li, Qi, Li & Peng, 2025 and *G. swinhonis* Günther, 1864 for the ND2 gene (Table 3). The Heishui population displayed substantial genetic divergence from all congeners, ranging from 8.2% (vs. *G. liboensis*) to 16.0% (vs. *G. swinhonis*) for the 16S gene and from 14.3% (vs. *G. fengshanensis*) to 25.2% (vs. *G. melli* (Vogt, 1922)) for the ND2 gene. In light of the well-supported monophyly, substantial genetic divergence, and distinct morphological characters that consistently differentiate the *Gekko* population from Sichuan Province from all known congeners (see Comparisons below), we herein describe the *Gekko* sp. from Heishui County, Sichuan Province, China, as a new species.

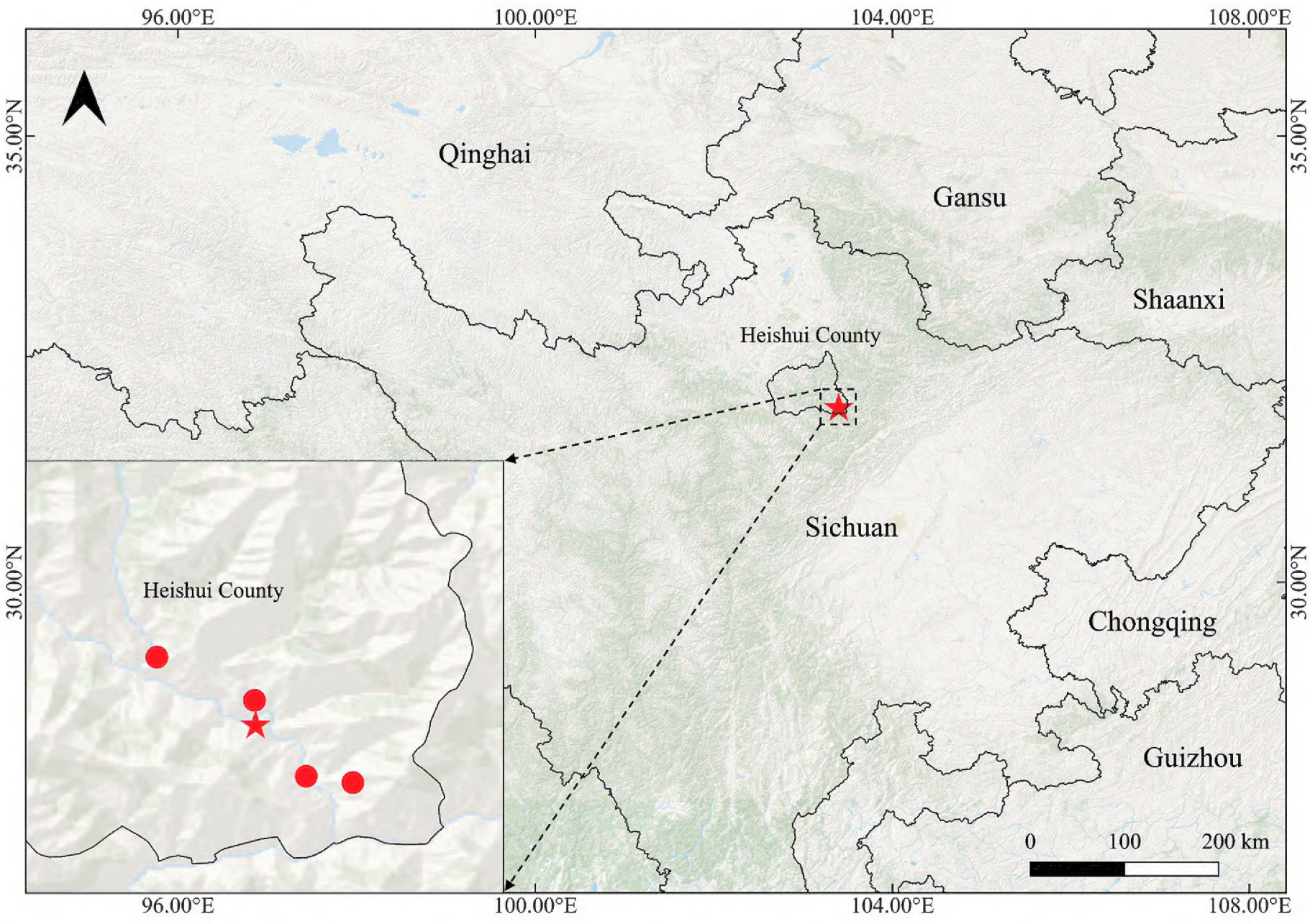

Figure 1. Map showing the locality of *Gekko tesselatus* sp. nov. The star indicates the type locality, and circles denote other known distribution sites.

Table 2. Uncorrected *p*-distances (%) of the 16S gene among species of *Japonigekko* used in this study.

NO	Species	1	2	3	4	5	6	7	8	9	10	11
1	*G. tesselatus* sp. nov.	0.0–0.8										
2	*G. adleri*	13.6–14.2	0.7									
3	*G. alpinus*	10.7–11.4	13.8–14.8	0.5								
4	*G. chinensis*	12.8–13.5	5.6–5.8	11.8–12.6	0.2							
5	*G. cib*	11.9–12.6	14.9	9.4–9.5	13.5–13.7	0.0						
6	*G. fengshanensis*	9.1–9.7	14.6–15.5	11.2–11.9	14.6–14.9	13.7–14.0	0.6					
7	*G. hokouensis*	11.3–11.9	14.2–14.4	12.0–13.1	12.8–13.2	13.2–13.4	12.6–13.1	0.4				
8	*G. ichangensis*	12.1–13.0	15.4	9.6–10.5	15.1–15.3	12.4–12.5	14.8–15.0	14.0–14.3	0.0			
9	*G. japonicus*	13.4–13.8	15.1–15.6	10.5–11.4	14.4–14.8	13.6–14.0	14.3–14.6	13.7–14.1	7.7–7.8	0.2		
10	*G. jinjiangensis*	9.5–9.8	13.0–13.4	4.0–4.4	11.3–11.5	10.2	12.0–12.2	10.0–10.2	9.9–10.0	10.8	–	
11	*G. kaiyai*	12.7–13.6	14.1–15.4	12.4–13.5	13.1–14.2	12.6–13.6	13.9–14.0	8.8–9.5	13.7–14.9	14.2–15.2	10.9–11.2	1.2
12	*G. kwangsiensis*	10.2–10.6	14.7	11.5–12.5	13.4–13.7	14.9–15.1	10.3–10.7	13.2–13.7	15.3–15.5	15.3–15.6	11.4–11.5	13.2–13.5
13	*G. liboensis*	8.2–9.2	14.2–15.2	11.3–12.4	13.8–14.2	13.3–13.5	9.0–9.4	14.6–14.7	14.4–14.6	13.3–13.7	12.4–12.6	14.3–15.2
14	*G. melli*	11.0–11.8	13.6–14.2	8.6–8.9	13.1–13.5	7.8–8.0	12.6–13.3	13.4–13.6	12.6	14.5–14.7	9.6–9.8	13.4–14.0
15	*G. palmatus*	13.1–13.5	2.5–2.9	13.2–14.0	3.8–4.4	13.7–14.1	15.3–15.6	12.6–13.2	15.4–15.8	13.7–14.1	12.3–12.7	13.6–14.0
16	*G. paucituberculatus*	8.9–9.3	14.0	10.5–11.2	12.5–12.7	12.9	10.7–10.9	11.7	16.0–16.1	15.4–15.5	10.2	12.9
17	*G. prep*	13.0–13.8	6.0–6.8	12.0–12.4	3.5–3.7	15.0–15.1	15.6–15.7	14.6–14.8	15.3–15.5	14.6–14.8	11.9–12.0	13.1–13.8
18	*G. similignum*	12.6–13.2	6.4	12.2–13.0	1.9–2.0	15.2	15.4–15.5	13.4–13.6	16.0–16.1	14.8–15.0	11.3	13.9–14.8
19	*G. scabridus*	11.0–11.2	13.5–13.9	4.7–4.9	12.2–12.4	9.7	11.5	11.1–11.3	11.5	11.1	5.4	11.2–11.5
20	*G. subpalmatus*	14.3–14.9	16.0	9.8–9.9	15.0–15.1	9.6	13.9–14.4	14.9–15.3	14.0	14.8–15.0	12.0	14.6–15.0
21	*G. swinhonis*	15.8–16.0	16.2–16.8	13.0–14.4	15.0–15.4	12.4–13.0	16.1–16.8	14.3–15.1	14.9–15.5	15.7–16.1	14.1–14.5	15.4–16.4

NO.	Species	12	13	14	15	16	17	18	19	20	21	
12	*G. kwangsiensis*	0.4										
13	*G. liboensis*	11.9–12.1	0.2									
14	*G. melli*	14.4–14.8	13.5–13.9	0.9								
15	*G. palmatus*	13.5–13.7	14.1–14.3	12.4–13.0	0.4							
16	*G. paucituberculatus*	12.0–12.3	9.6–9.8	13.1–13.3	12.0–12.2	0.0						
17	*G. prep*	13.6–13.8	15.0–15.2	13.7–13.9	4.2–4.6	14.0	0.2					
18	*G. similignum*	14.2–14.3	14.2–14.4	13.7–14.3	4.6–5.0	14.0	4.3	0.0				
19	*G. scabridus*	12.1–12.4	12.2	10.0–10.2	12.6–13.1	10.6	12.6–12.7	12.4	–			
20	*G. subpalmatus*	13.4–13.6	15.5–15.7	8.8–9.0	14.1–14.5	15.1	14.8	15.7	12.0	–		
21	*G. swinhonis*	16.0–16.3	15.1–15.5	14.3–14.8	14.6–15.0	15.8–16.2	15.4–16.0	15.4–15.9	14.9–15.1	13.9–14.4	1.1	

Table 3. Uncorrected *p*-distances (%) of the ND2 gene among species of *Japonigekko* used in this study.

NO.	Species	1	2	3	4	5	6	7	8	9	10	11	12	13
1	*G. tesselatus* sp. nov.	0.0–1.0												
2	*G. adleri*	23.8–25.0	–											
3	*G. alpinus*	19.6–20.9	23.4–23.6	1.6										
4	*G. auriverrucosus*	19.6–20.5	24.8	21.5–22.2	–									
5	*G. bonkowskii*	20.3–20.7	24.6	19.0–19.4	21.5	–								
6	*G. chinensis*	22.5–24.5	14.4–14.6	21.9–22.7	24.3–24.5	21.2–21.4	0.4							
7	*G. cib*	22.1–22.7	26.1	22.2–22.8	20.7	19.4	24.0–24.3	0.0						
8	*G. fengshanensis*	14.3–14.9	23.4	20.0–20.3	22.1	19.6	23.7	21.7	0.0					
9	*G. hokouensis*	19.7–21.2	24.8–25.2	19.9–21.6	21.0–21.5	19.0–20.3	24.2–25.0	23.0–23.6	20.6–20.9	1.3				
10	*G. japonicus*	20.3–21.8	26.1	19.6–20.6	20.9	19.6	24.9–25.2	22.9	21.4	22.5–22.7	0.0			
11	*G. jinjiangensis*	16.9–17.2	20.7–21.3	7.1–8.4	19.9–20.5	17.9–19.0	21.1–22.4	20.6–20.7	17.0–18.3	18.0–20.4	16.9–17.2	2.4		
12	*G. khunkhamensis*	22.4–22.8	26.0	21.3–21.7	24.3	15.2	24.6–24.8	21.1	22.2	23.8–24.2	22.6	20.9–21.7	–	
13	*G. kwangsiensis*	16.6–17.4	24.1–24.2	21.8–22.7	22.4–22.5	20.9–21.0	23.0–23.3	20.7–20.9	15.9–16.1	21.4–21.8	22.7–22.8	19.1–19.4	21.5–21.7	0.4
14	*G. liboensis*	16.4–16.7	23.4–23.5	20.8–21.7	22.1–22.2	19.4–19.6	24.7–24.9	21.4–21.5	17.0–17.1	19.6–20.2	22.8–22.9	19.3–20.0	21.5–21.7	18.1–18.4
15	*G. melli*	23.4–25.2	24.5–25.1	21.9–23.0	22.6–23.5	21.2–21.8	24.7–25.2	18.9–19.0	24.1–24.3	23.6–24.6	23.6–23.8	19.3–21.1	23.4	23.3–23.8
16	*G. nadenensis*	21.6–22.0	23.3	18.6–19.4	20.2	6.9	21.2–21.8	20.3	20.5	21.2–22.2	19.9	16.9–18.1	13.8	20.5–20.7
17	*G. palmatus*	22.3–24.2	6.5	22.4–22.6	23.6–23.8	23.1–23.6	14.3–14.4	25.9–26.1	23.1–23.2	23.7–24.4	24.9–25.0	20.7–21.1	25.6–26.2	23.4–23.5
18	*G. paucituberculatus*	14.9–16.6	25.3–25.4	19.4–20.4	21.2–21.3	19.2	25.4–25.5	21.0–21.1	17.4–17.5	21.0–21.8	21.7–21.8	17.2–17.6	21.5	19.0–19.3
19	*G. prep*	23.1–24.7	15.9–16.0	24.6–25.6	26.1–26.3	21.6–22.2	7.4–8.0	24.8–24.9	25.0	25.6–26.0	26.4–26.7	22.6–23.5	25.4–25.6	24.2–24.4
20	*G. scientiadventura*	20.1–20.5	24.4	18.4–18.8	20.4	13.8	22.5	20.5	19.6	21.4–21.6	21.0	17.7	14.8	20.9
21	*G. sengchanthavongi*	19.4	23.8	20.0–20.2	20.0	14.2	22.2–22.7	21.6	20.1	22.0–22.9	20.9	19.0–19.2	15.7	21.4
22	*G. similignum*	22.5–24.0	15.0–15.1	22.6–23.3	25.3–25.4	22.9–23.1	5.4–5.5	25.3–25.4	24.0–24.1	24.6–25.1	25.0–25.1	21.3–22.2	24.8–25.0	23.5–23.6
23	*G. scabridus*	17.4–17.8	18.3–19.1	11.5–12.6	19.2–19.7	19.9–20.3	20.2–20.7	21.1–21.7	16.7	17.0–17.4	17.2–17.6	9.6–11.5	21.7–22.6	20.2–20.9
24	*G. subpalmatus*	21.3–22.4	25.0	21.7–22.2	21.6	20.5	24.1–24.4	17.9	21.7	23.3–23.4	23.1	19.1–20.2	22.6	22.2
25	*G. swinhonis*	20.2–20.9	25.1	22.6–22.7	20.7	21.2	25.7–25.8	21.9	20.7	22.0–22.5	21.9	20.4	23.6	21.8–21.9
26	*G. thakhekensis*	20.9–21.2	21.8	19.0–19.6	20.6	6.7	19.9–20.5	20.3	19.4	20.5–20.9	19.0	18.1–19.2	15.9	20.1–20.3
27	*G. truongi*	22.9	20.5	20.2–20.3	24.3	22.0	20.9–21.2	21.8	23.6	22.3	21.8	19.6–19.9	22.2	22.7–22.9

NO.	Species	14	15	16	17	18	19	20	21	22	23	24	25	26
14	*G. liboensis*	0.1												
15	*G. melli*	23.9–24.5	2.7											
16	*G. nadenensis*	18.8–19.0	20.1–21.4	–										
17	*G. palmatus*	23.2–23.4	25.2–25.9	22.5–23.2	1.2									
18	*G. paucituberculatus*	17.8–18.0	25.0–25.3	18.6	24.4–24.5	0.1								
19	*G. prep*	26.2–26.3	26.4–27.0	22.3–22.9	15.2–15.4	26.4–26.5	0.4							
20	*G. scientiadventura*	20.3–20.5	21.2–21.6	13.4	22.9–23.5	18.6	23.8–24.4	–						
21	*G. sengchanthavongi*	19.7–19.9	21.8–22.5	11.9	23.5	19.0	22.7–23.3	10.4	–					
22	*G. similignum*	24.5–24.7	25.8–26.4	22.5–22.7	13.9–14.5	24.9–25.0	8.5–9.0	22.9–23.1	22.5–22.7	0.1				
23	*G. scabridus*	16.9–18.3	19.3–21.3	19.2–19.6	19.7–20.2	17.8	21.9–22.4	17.1–18.8	18.4–19.2	20.2–21.1	1.5			
24	*G. subpalmatus*	21.4–21.5	17.8–18.4	18.6	25.3–25.5	22.4–22.5	25.5–25.6	20.3	20.5	25.0–25.1	20.0–21.1	0.0		
25	*G. swinhonis*	21.9–22.0	23.1–23.4	21.4	24.0–24.3	23.7–23.8	26.5–26.7	22.5	22.2	25.5–25.6	19.6–20.2	21.8	–	
26	*G. thakhekensis*	18.6–18.8	19.7–20.7	6.7	22.2–22.9	18.1	21.6–22.2	13.0	13.0	20.9–21.0	19.0–19.4	19.9	23.1	–
27	*G. truongi*	21.8–22.0	20.7–21.4	22.0	21.6–21.8	21.2	22.2–22.7	22.2	21.8	21.6–21.8	18.2–19.7	21.4	24.0	20.3

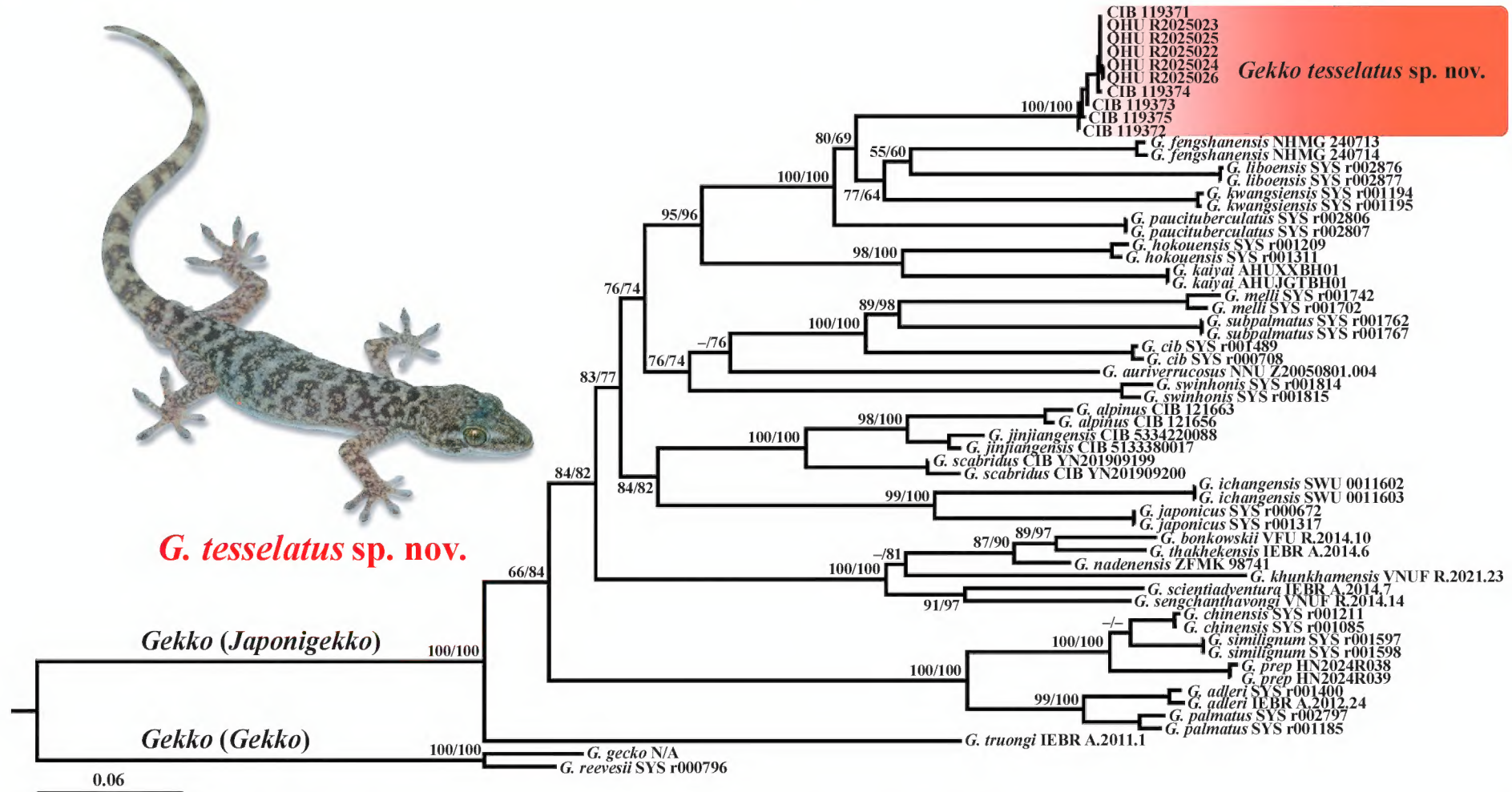

Figure 2. Maximum likelihood (ML) tree of *Japonigekko* inferred from 16S and ND2 genes. Node support values are presented as SH-like approximate likelihood ratio test (SH)/ultrafast bootstrap approximation (UFB); those lower than 50 are shown as "–". Photograph on thumbnail by YHX.

Taxonomic account

Family Gekkonidae Oppel, 1811
Genus *Gekko* Laurenti, 1768
Subgenus *Japonigekko* Wood, Guo, Travers, Su, Olson, Bauer, Grismer, Siler, Moyle, Andersen & Brown, 2020

***Gekko tesselatus* Xu, Ma, Cai, Qi, Matsukoji, Poyarkov, Sun, Jiang & Peng, sp. nov.**

https://zoobank.org/6373BF5E-F05B-4248-8B7D-0E50B1E10BE3

Figs 3–10, Tables 4–6

Type material. ***Holotype*** • CIB 119371 (Field no. LFR 2025142), adult male, from Se'ergu Town, Heishui County, Aba Tibetan and Qiang Autonomous Prefecture, Sichuan Province, China (31.9531°N, 103.3971°E; 1,847 m asl.), collected by Yuhao Xu, Fanyue Sun, and Jiaxiang Wu on 3 August 2025.

***Paratypes* (N = 13, all from Sichuan Province, China)** • QHU R2025022 (Field no. LFR 2025143, adult female) • QHU R2025023 (Field no. LFR 2025144, adult male) • QHU R2025024 (Field no. LFR 2025145, adult female), with the same collecting information as the holotype • QHU R2025025 (Field no. LFR 2025146, adult male), from Longba Town, Heishui County (31.9855°N, 103.3503°E; 2,047 m asl.), collected by Yuhao Xu, Fanyue Sun and Jiaxiang Wu on August 04, 2025 • QHU R2025026 (Field no. LFR 2025147, subadult male), from Se'ergu Town, Heishui County (31.9290°N, 103.4211°E; 1,827 m asl.), collected by Yuhao Xu, Fanyue Sun and Jiaxiang Wu on August 4, 2025 • SYS r003029 (Field no. LFR 2025148, adult male) • SYS r003030 (Field no. LFR 2025149, adult female), from Se'ergu Town, Heishui County (31.9260°N, 103.44324°E; 1,886 m asl.), collected by Yuhao Xu, Fanyue Sun and Jiaxiang Wu on August 4, 2025 • SYS r003031 (Field no. LFR 2025150, adult female) • SYS r003032 (Field no. LFR 2025151, subadult female), from the same locality as the holotype, collected by Yuhao Xu, Fanyue Sun and Jiaxiang Wu on August 4, 2025 • CIB 119372 (adult female) • CIB 119373 (adult female) • CIB 119374 (adult female) • CIB 119375 (subadult female), from Se'ergu Town, Heishui County (31.9650°N, 103.3966°E; 1,938 m asl.), collected by Bo Cai in July, 2025.

Etymology. The specific name "*tesselatus*" is a Latinized adjective in the nominative singular (masculine gender), derived from "*tessella*" (a small square tile), and means "reticulated" or "checkerboard-like." It refers to the characteristic dorsal pattern of the new species, which consists of a series of irregular dark transverse bands that are faintly interrupted medially by a narrow vertebral line and, laterally, are partly fragmented and partly interconnected, forming an irregular, checkerboard-like reticulated pattern across the dorsum. For the common names, we suggest "Checkered Gecko" in English and "Bān Wén Bì Hǔ" (斑纹壁虎) in Chinese.

Diagnosis. *Gekko tesselatus* sp. nov. can be diagnosed from other *Japonigekko* species by the following unique combination of characters: (1) a moderate body size (SVL reaches up to 64.9 mm in males and 72.9 mm in females); (2) nares in contact with the rostral, internasal 0 or 1; (3) two enlarged postmentals, rarely one; (4) flattened dorsal tubercles present from the posterior head through the neck to the anterior portion of the tail, arranged in 12–15 rows

at midbody; (5) 130–157 ventral scales between the mental and the cloacal slit; (6) 98–106 midbody scale rows; (7) 31–39 ventral scale rows; (8) subdigital lamellae 7–10 on finger I, 9–12 on finger IV, 7–9 on toe I, and 9–12 on toe IV; (9) webbing absent; (10) 6–8 precloacal pores in males, absent in females; (11) one postcloacal tubercle on each side, rarely two; (12) in life, the dorsum is predominantly greyish brown, with a series of irregular dark transverse bands that are faintly interrupted medially by a narrow vertebral stripe and laterally fragmented and interconnected, forming an irregular, checkerboard-like reticulated pattern.

Description of the holotype. (Fig. 3). An adult male specimen with original tail. Size medium, SVL 61.4 mm; body slender and trunk relatively elongate, AGD 29.0 mm, AGD/SVL ratio 0.47; tail slightly longer than body, distinctly swollen at base, oval in section, TAL 72.3 mm, TAL/SVL ratio 1.19.

Head depressed, noticeably longer than wide, and clearly separated from the neck, HL 17.09 mm, HW 12.31 mm, HH 5.00 mm, HH/HL ratio 0.29, HL/HW ratio 1.39. Snout obtuse, round anteriorly, ESD 7.14 mm, ESD/HL ratio 0.42. Eye large, ED 3.89 mm, ED/HL ratio 0.23; pupil vertical, featuring crenulated edges. Ear opening small, approximately elliptical, obliquely oriented, EL 1.12 mm, EL/ED ratio 0.29.

Rostral approximately rectangular in shape, wider than the high, RW 2.31 mm, RH 1.46 mm, RW/RH ratio 1.58. Nares oval, rounded by the rostral, 1st supralabial, one distinctly enlarged supranasal, and three slightly enlarged nasals posteriorly; internasals absent. Preorbitals 18/17, preorbital region deeply concave; interorbital scales between the anterior corners of eyes 24; supralabials 10/10; infralabials 9/9. Mental pentagonal, wider than long, MW 1.80, ML 1.42, MW/ML ratio 1.27; mental narrower than the rostral, RW/MW ratio 1.28; postmentals two, enlarged, twice as long as wide, touching the mental and the first infralabial on both sides and three gular scales posteriorly. Tubercles present on the dorsal surface of the head behind the eyes; granular scales on the anterodorsal region of the head are larger than those on the posterior region.

Dorsal scales smooth, round to oval, granular, and juxtaposed; tubercles flattened, irregularly arranged, extending from the posterior part of the head to the anterior one-third of the tail, forming approximately 14 rows at midbody, surrounded by 8–9 dorsal scales. Ventrolateral fold present, without tubercles; ventrals slightly larger than dorsals, smooth, imbricate, and largest in middle of belly; ventral scale rows at midbody 36; scale rows around midbody 106; ventral scales in a row between mental and cloacal slit 138; precloacal scales enlarged, but no enlarged scales on thighs; precloacal pores 6 (Fig. 4A), situated at the distal of each scale, the tips of the two central scales are slightly inclined laterally, separating the precloacal pores at the midline into two groups (3/3); postcloacal tubercle 1/1 (Fig. 5A), large, surrounded by several smaller tubercles delineated by shallow grooves. Dorsal scales of tail flat and smooth, irregular in size, with a few tubercles present on the anterior one-third of the tail; subcaudals small at the base, distinctly enlarged beyond the swollen portion, and arranged in a longitudinal row.

Forelimbs and hindlimbs well developed; dorsal surface of forelimbs without tubercles, but dorsal surface of hindlimbs bearing tubercles; no webbing between the fingers and toes; digits moderately dilated; fingers and toes II–IV clawed; claws laterally compressed, extending beyond the terminal lamellae; no webbing between fingers and toes; subdigital lamellae undivided, under manus 7-9-10-11-9 (left) / 7-8-9-11-9 (right), and under pes 8-8-10-11-8 (left) / 8-8-11-11-10 (right); relative length of fingers and toes I < II < V < III < IV.

Coloration of the holotype in life. (Fig. 6). In life, the dorsal ground color of the head and body is light greyish-brown, scattered with small dark brown to yellowish-brown spots. A faint W-shaped dark marking extending anteriorly from the occipital region to the posterior corners of the eyes. On the lateral sides of the head, a dark longitudinal stripe running from the posteroventral corner of the eye to the ear opening. Eight irregular dark transverse bands between the nape and the sacrum. The dark bands faintly divided along the midline by a narrow, light-colored vertebral line running intermittently from the nape to the tail tip. Laterally, the bands partly fragmented and interconnected, forming an irregular reticulated pattern reminiscent of a checkerboard. All dark markings and bands consist of a mixture of yellowish-brown and dark brown spots. The dorsal surfaces of the limbs bearing irregular dark transverse or reticulated markings. The tail light greyish-brown at the base, gradually becoming paler posteriorly, and bearing 12 dark transverse bands; the tail tip dark brown. The head and ventral surfaces of the body uniformly creamy white, while the ventral surface of the tail pale yellowish-white.

After capture, the overall body color becomes paler, turning yellowish-brown, and the dark markings on the dorsum become blurred. However, after being kept in captivity for several days, the color pattern gradually returns to its original state, even when housed in a white container.

Coloration of the holotype in preservation. (Fig. 3). In preservative, the dorsal ground color of the head, body, and limbs turns grey, with the yellowish-brown spots on the dorsum disappearing, while the dark brown markings remained distinct; the ventral surface faded to greyish-white.

Variation. The main morphological characters of *Gekko tesselatus* sp. nov. are summarized in Table 4. The species exhibits no evident sexual dimorphism in morphometric ratios, scale counts, or coloration. The longest known male measures SVL 64.9 mm, with TAL 72.9 mm (QHU R2025025); and the female measures SVL 65.3 mm, with TAL 65.1+ mm (QHU R2025022); TAL/SVL ratio 1.07–1.23. Head depressed, noticeably longer than wide, and clearly separated from the neck, HL/HW ratio 1.16–1.47. Snout obtuse, round anteriorly, ESD/HL ratio 0.38–0.43. Eye large; pupil vertical, featuring crenulated edges. Ear opening small, approximately elliptical, obliquely oriented, EL/ED ratio 0.19–0.40, and EL/HL ratio 0.04–0.08.

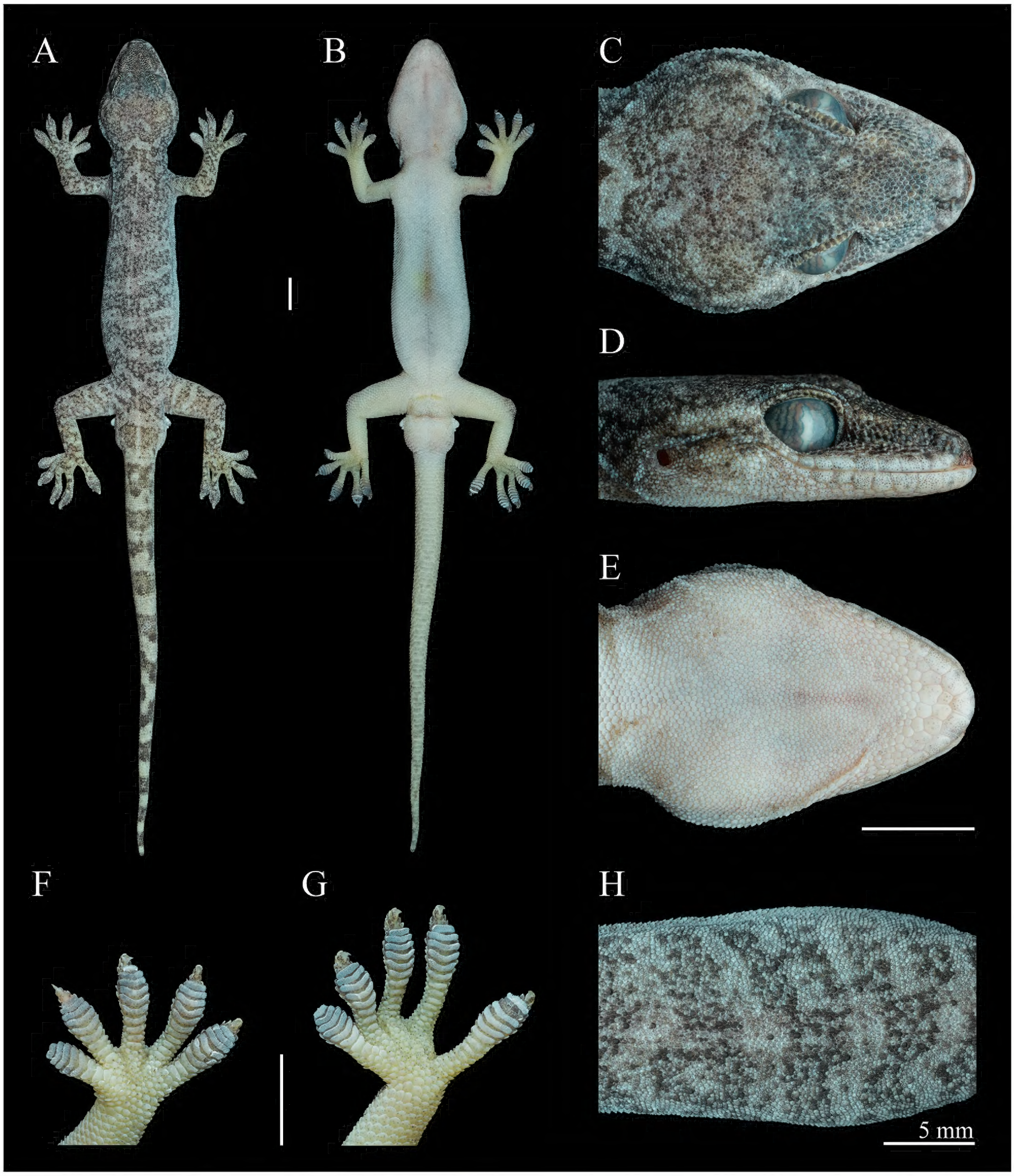

Figure 3. Preserved specimen of the holotype of *Gekko tesselatus* sp. nov. (CIB 119371, male). **A.** Dorsal view; **B.** Ventral view; **C.** Dorsal view of head; **D.** Lateral view of head; **E.** Ventral view of head; **F.** Ventral view of hand; **G.** Ventral view of foot; **H.** Dorsal view of midbody. Photographs by YHX. Scale bars: 5 mm.

Rostral rectangular in shape, wider than high; NS 3 or 4; INS 0 or 1; PO 12–15, preorbital region deeply concave; IOS 24; SL 10 or 11; IL 9–12. Mental pentagonal, narrower than the rostral; PM 2 (1 in specimen SYS r003031); GP 3–6. Dorsal scales smooth, round to oval, granular, and juxtaposed, MBSR 98–106; tubercles flattened, irregularly arranged, extending from the posterior part of the head to the anterior part of the tail, DTR 12–15, GSDT 7–9; ventrals slightly larger than dorsals, smooth, imbricate, and largest in middle of belly, VS 31–39, SMC 130–157; precloacal scales enlarged, but no enlarged scales on thighs. PP 6–8 in males, situated at the distal of each scale; in CIB 119371, QHU R2025026, and SYS r003029, the tips of the two central scales are laterally inclined, separating the precloacal pores into two groups (3/3); QHU R2025023 also has 6 PP (3/3),

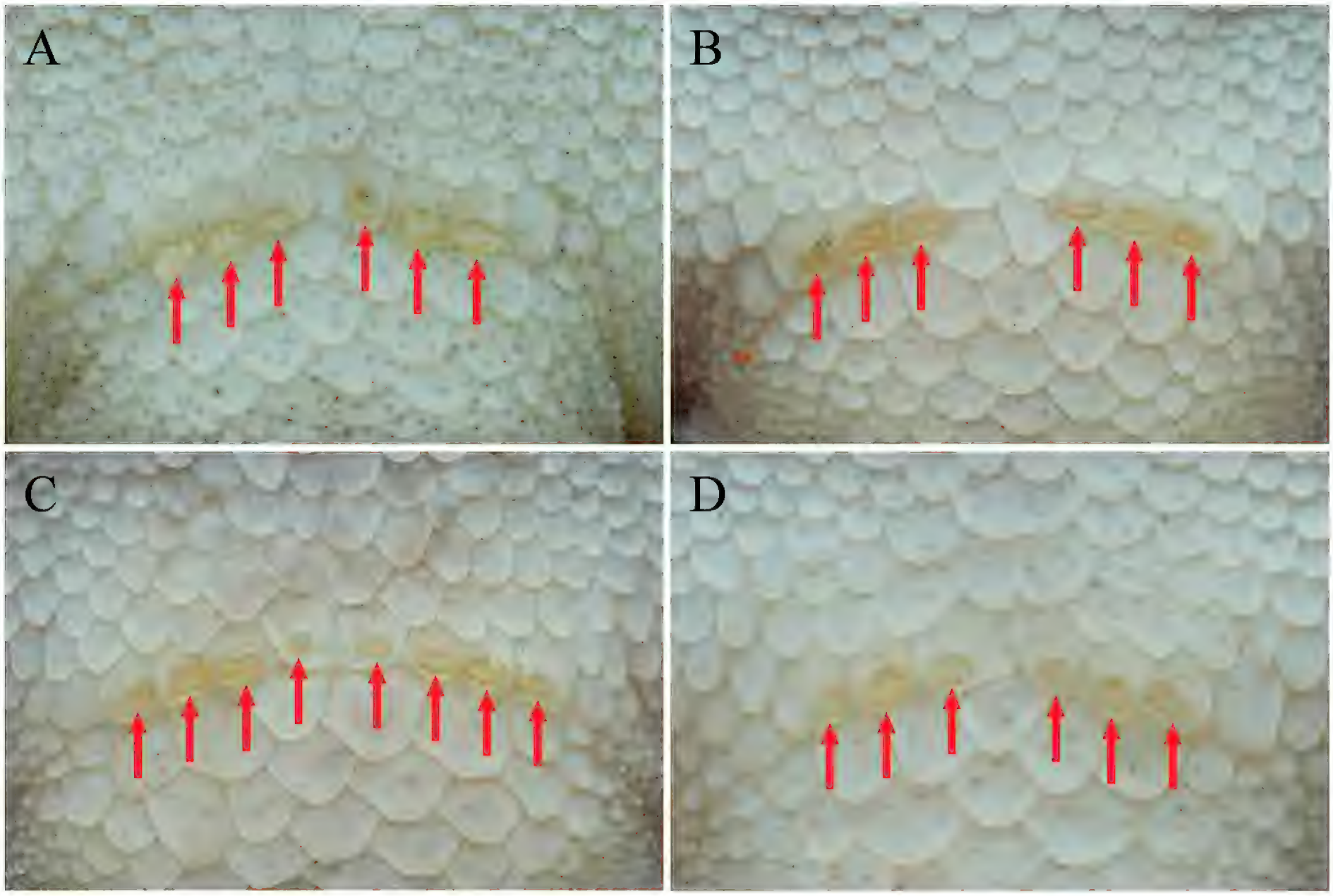

Figure 4. Precloacal pores in the adult male *Gekko tesselatus* sp. nov. **A.** Specimen CIB 119371, holotype; **B.** Specimen QHU R2025023, paratype; **C.** Specimen QHU R2025025, paratype; **D.** Specimen SYS r003029, paratype. Photographs by YHX.

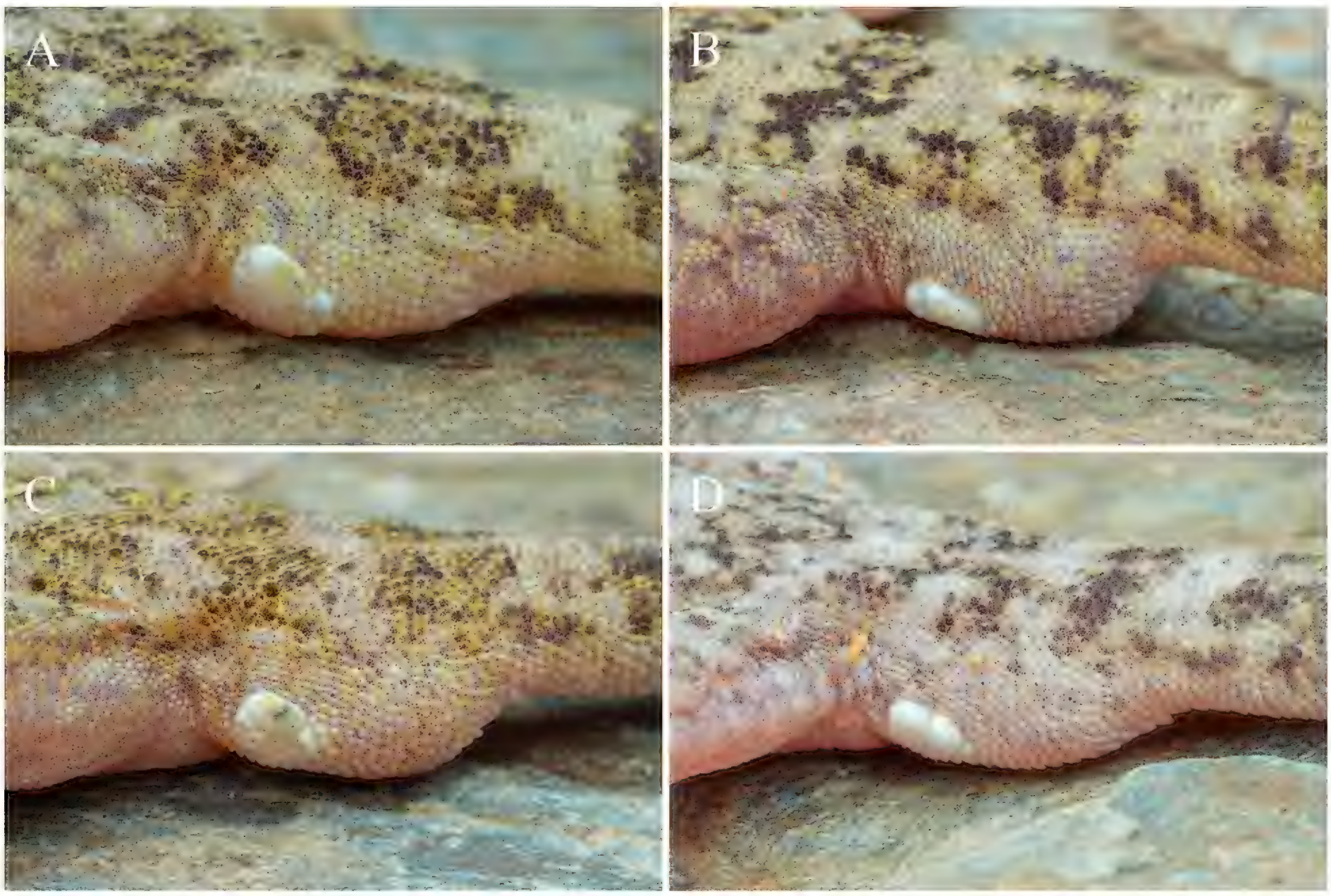

Figure 5. Postcloacal tubercles in the adult male *Gekko tesselatus* sp. nov. **A.** Specimen CIB 119371, holotype; **B.** Specimen QHU R2025023, paratype; **C.** Specimen QHU R2025025, paratype; **D.** Specimen SYS r003029, paratype. Photographs by YHX.

Figure 6. Holotype of *Gekko tesselatus* sp. nov. in life. **A.** Dorsal view; **B.** Ventral view; **C.** Dorsal view of head; **D.** Lateral view of head; **E.** Ventral view of head. Photographs by YHX.

but the central are separated by two intervening scales; in QHU R2025025, all 8 PP are arranged continuously (Fig. 4); PP absent in females. PAT 1 on each side (2 on the left side only in specimen SYS r003029), large in males and surrounded by several smaller tubercles delineated by shallow grooves (Fig. 5); in females, the postcloacal tubercles are smaller and less distinct. Dorsal scales of tail flat and smooth, irregular in size, with a few tubercles present on the anterior part of the tail; subcaudals small at the base, distinctly enlarged beyond the swollen portion, and arranged in a longitudinal row.

Forelimbs and hindlimbs well developed; dorsal surface of forelimbs without tubercles, but dorsal surface of hindlimbs bearing tubercles; no webbing between the fingers and toes; digits moderately dilated; fingers and toes II–IV clawed; claws laterally compressed, extending beyond the terminal lamellae; LF1 7–10; LF4 9–12; LT1 7–9; LT4 9–12.

Main characters of the pattern in life. (Fig. 7). In life, the coloration of the paratypes resembles that of the holotype. The dorsal surface of the body consists of 7–10 irregular dark transverse bands, which are faintly interrupted along the midline by a narrow vertebral line. Laterally, these bands are partly fragmented and partly interconnected, forming an irregular, checkerboard-like reticulated pattern across the dorsum. The dorsal surface of the tail (based only on original tail specimens) bears 11–14 relatively regular dark transverse bands, forming distinct annulations. The ventral surface of the body is uniformly creamy white, while the ventral surface of the tail is pale yellowish-white.

Main characters of the pattern in preservation. (Fig. 8). In preservative, the dorsal ground color of the head, body, and limbs turns grey or greyish-white, with the yellowish-brown spots on the dorsum disappearing, while the dark brown markings remain distinct; the ventral surface fades to greyish-white.

Distribution and habitat. *Gekko tesselatus* sp. nov. is currently known only from its type locality, Se'ergu Town, Heishui County, northwestern Sichuan Province, China. All individuals were collected at night from rocky slopes within a hot-dry valley covered with low shrubs and grasses, at elevations between 1,827 m and 2,047 m, where nighttime temperatures remained above 26 °C (Fig. 9A, B). Field observations indicate that this species shows a strong preference for heavily weathered rock faces with abundant crevices (Fig. 9C). Individuals were usually hiding in crevices more than two meters

Table 4. Measurements (in mm), body proportions, and scalation features of the type series of *Gekko tesselatu* sp. nov. See the Materials and methods section for abbreviations. "–" unavailable data. Bilateral scale counts are given as left/right.

Voucher Number	CIB 119371	CIB 119372	CIB 119373	CIB 119374	CIB 119375	QHU R2025022	QHU R2025023	QHU R2025024
Type	Holotype	Paratype	Paratype	Paratype	Paratype	Paratype	Paratype	Paratype
Sex	Male	Female	Female	Female	Juvenile female	Female	Male	female
SVL	61.4	58.3	52.2	58.3	37.4	65.3	60.7	63.8
TAL	72.3	66.6	58.4	53.5+	41.9	65.1+	69.8	69.9
TAL/SVL	1.18	1.14	1.12	–	1.12	–	1.15	1.10
AGD	29.0	29.3	25.0	26.4	16.7	30.6	29.8	32.3
AGD/SVL	0.47	0.50	0.48	0.45	0.45	0.47	0.49	0.51
HL	17.09	15.76	14.62	15.33	10.97	16.20	14.97	15.24
HW	12.31	11.46	11.07	10.68	8.45	13.69	12.30	13.12
HH	5.00	5.32	5.44	4.34	3.86	7.08	6.62	5.97
HL/SVL	0.28	0.27	0.28	0.26	0.29	0.25	0.25	0.24
HL/HW	1.39	1.38	1.32	1.44	1.30	1.18	1.22	1.16
ESD	7.14	6.08	6.14	6.51	4.50	6.16	5.98	6.03
ED	3.89	3.05	2.94	3.06	2.22	3.69	3.37	4.06
ESD/HL	0.42	0.39	0.42	0.42	0.41	0.38	0.40	0.40
ESD/ED	1.84	1.99	2.09	2.13	2.03	1.67	1.77	1.49
EL	1.11	1.22	1.02	1.07	0.64	1.13	1.22	0.96
EL/ED	0.29	0.40	0.35	0.35	0.29	0.31	0.36	0.24
EL/HL	0.06	0.08	0.07	0.07	0.06	0.07	0.08	0.06
RW	2.31	3.12	2.97	3.07	2.29	2.87	2.78	2.83
RH	1.46	1.20	1.12	1.23	1.09	1.39	1.66	1.65
RW/RH	1.58	2.60	2.65	2.50	2.10	2.06	1.67	1.72
MW	1.8	2.26	2.28	2.04	1.44	1.61	1.40	1.54
ML	1.42	1.22	1.23	1.21	0.94	1.36	1.20	1.47
MW/ML	1.27	1.85	1.85	1.69	1.53	1.18	1.17	1.05
RW/MW	1.28	1.38	1.30	1.50	1.59	1.78	1.99	1.84
NS	4/4	3/3	3/3	3/3	3/3	3/3	3/3	4/4
INS	0	0	0	0	0	1	1	1
SL	10/10	10/10	10/10	10/10	10/10	10/10	11/11	11/11
IL	9/9	9/9	9/9	9/9	9/9	10/9	11/10	10/12
IOS	22	24	25	26	26	24	24	22
PO	14/13	13/14	15/15	14/13	15/14	15/14	13/13	15/13
PM	2	2	2	2	2	2	2	2
GP	3	4	4	6	5	4	5	5
DTR	14	14	15	15	14	14	13	15
GSDT	8–9	7–9	7–9	7–9	7–9	8–9	7–9	8–9
SMC	138	130	157	147	138	154	142	147
MBSR	106	105	98	105	103	105	100	100
VS	36	39	37	35	34	31	34	31
LF1	7/7	7/8	8/8	7/7	7/7	8/7	8/8	10/9
LF4	11/11	10/10	11/11	11/11	9/9	10/10	10/10	10/12
LT1	8/8	9/9	8/8	7/7	8/8	8/8	8/–	7/8
LT4	11/11	12/12	11/11	11/11	11/11	10/10	10/10	11/9
PP	6	0	0	0	0	0	6	0
PAT	1/1	1/1	1/1	1/1	1/1	1/1	1/1	1/1
Web	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
Fore tubercles	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
Hind tubercles	Present	Present	Present	Present	Present	Present	Present	Present
Tail tubercles	Present	Present	Present	Present	Present	Present	Present	Present

Voucher Number	QHU R2025025	QHU R2025026	SYS r003029	SYS r003030	SYS r003031	SYS r003032	Range
Type	Paratype	Paratype	Paratype	Paratype	Paratype	Paratype	
Sex	Male	Subadult male	Male	Female	Female	Subadult female	–
SVL	64.9	52.4	58.8	61.9	63.4	54.2	37.4–65.3
TAL	72.9	56.3	72.2	55.3+	68.4	61.2	41.9–72.9
TAL/SVL	1.12	1.07	1.23	–	1.08	1.13	1.07–1.23
AGD	31.8	25.3	29.42	29.26	32.33	26.51	16.70–32.33
AGD/SVL	0.49	0.48	0.50	0.47	0.51	0.49	0.45–0.51
HL	16.18	13.25	15.57	16.10	16.90	15.25	10.97–17.09
HW	13.29	10.77	11.83	12.22	12.70	10.37	8.45–13.69
HH	5.71	5.04	5.53	5.90	5.66	4.68	3.86–7.08
HL/SVL	0.25	0.25	0.26	0.26	0.27	0.28	0.24–0.29
HL/HW	1.22	1.23	1.32	1.32	1.33	1.47	1.16–1.47
ESD	6.61	5.28	6.57	6.91	6.75	5.82	4.50–7.14
ED	3.41	3.28	3.89	3.52	3.86	3.28	2.22–4.06
ESD/HL	0.41	0.40	0.42	0.43	0.40	0.38	0.38–0.43
ESD/ED	1.94	1.61	1.69	1.96	1.75	1.77	1.49–2.13
EL	1.07	0.87	0.78	0.80	0.76	0.61	0.61–1.22
EL/ED	0.31	0.27	0.20	0.23	0.20	0.19	0.19–0.40
EL/HL	0.07	0.07	0.05	0.05	0.04	0.04	0.04–0.08
RW	2.66	1.98	2.52	2.48	2.83	2.27	1.98–3.12
RH	1.55	1.12	1.18	1.32	1.30	1.14	1.09–1.66
RW/RH	1.72	1.77	2.14	1.88	2.18	1.99	1.58–2.65
MW	1.66	1.32	1.57	1.58	1.58	1.50	1.32–2.28
ML	1.63	1.26	1.38	1.21	1.04	1.02	0.94–1.63
MW/ML	1.02	1.05	1.14	1.31	1.52	1.47	1.02–1.85
RW/MW	1.60	1.50	1.61	1.57	1.79	1.51	1.28–1.99
NS	3/3	4/4	3/3	3/3	4/4	3/3	3 or 4
INS	1	0	1	1	1	0	0 or 1
SL	11/10	11/11	11/11	10/10	10/10	10/10	10 or 11
IL	12/10	11/10	10/10	11/11	11/10	9/9	9–12
IOS	22	23	22	24	22	22	22–26
PO	13/12	14/14	14/14	15/15	14/15	13/14	12–15
PM	2	2	2	2	1	2	2 (rarely 1)
GP	4	4	5	5	3	4	3–6
DTR	14	15	14	12	13	12	12–15
GSDT	7–9	8–9	8–9	8–9	8–9	8–9	7–9
SMC	157	149	137	147	151	150	130–157
MBSR	98	102	100	103	100	101	98–106
VS	32	33	35	35	36	36	31–39
LF1	9/8	9/8	9/9	10/9	9/9	8/7	7–10
LF4	10/11	10/10	11/11	11/11	10/11	10/11	9–12
LT1	8/8	8/8	9/9	9/8	9/8	9/8	7–9
LT4	11/11	11/11	10/12	11/10	11/10	10/11	9–12
PP	8	6	6	0	0	0	6–8 in males
PAT	1/1	1/1	2/1	1/1	1/1	1/1	1 (rarely 2)
Web	Absent	Absent	Absent	Absent	Absent	Absent	Absent
Fore tubercles	Absent	Absent	Absent	Absent	Absent	Absent	Absent
Hind tubercles	Present	Present	Present	Present	Present	Present	Present
Tail tubercles	Present	Present	Present	Present	Present	Present	Present

above the ground, with scattered feces observed nearby. By contrast, on less weathered slopes with few crevices, individuals were rarely encountered. The highest altitude at which specimens were collected was 2,047 m, where only a single individual was found despite the high degree of rock weathering. No traces of the species were detected at higher elevations, suggesting that its actual altitudinal range may not exceed 2,100 m. The lower temperatures at higher elevations are likely unsuitable for its survival.

Figure 7. Coloration of *Gekko tesselatus* sp. nov. in life. **A.** Specimen QHU R2025022, adult female; **B.** Specimen QHU R2025023, adult male; **C.** Specimen QHU R2025024, adult female; **D.** Specimen QHU R2025025, adult male; **E.** Specimen QHU R2025026, subadult male; **F.** Specimen SYS r003029, adult male. Photographs by YHX.

In addition, the species appears to be poorly adapted to anthropogenically modified environments. Although some collection sites were located close to villages, no individuals were observed around human dwellings. Within the same habitat, we also recorded *Lycodon multizonatus* (Zhao & Jiang, 1981), which may represent one of the principal natural predators of *Gekko tesselatus* sp. nov. (Fig. 9D).

Comparisons. Based on both morphological and molecular evidence, *Gekko tesselatus* sp. nov. is closely related to *G. fengshanensis*, *G. kwangsiensis*, *G. liboensis*, and *G. paucituberculatus*. Detailed morphological comparisons between *Gekko tesselatus* sp. nov. and four closest species are shown in Table 5 and Fig. 10. *Gekko tesselatus* sp. nov. can be distinguished from *G. fengshanensis* by (1) MBSR 98–106 (vs. 149–161), (2) VS 31–39 (vs. 40–49), (3) SMC 130–157 (vs. 197–213), (4) DTR 12–15 (vs. 9–11), (5) PP 6–8 (vs. 9–12), (6) LF1 7–10 (vs. 11–13), (7) LT1 7–9 (vs. 12–14), and (8) LT4 9–12 (vs. 13–15). It can be distinguished from *G. kwangsiensis* by (1) MBSR 98–106 (vs. 143–156), (2) VS 31–39 (vs. 41–45), (3) SMC 130–157 (vs. 185–208), (4) DTR 12–15 (vs. 9–11), (5) PP 6–8 (vs. 9–10), (6) LT1 7–9 (vs. 11–13), (7) IOS 24–28 (vs. 29–31), and (8) LT4 9–12 (vs. 14–18). It can be distinguished from *G. liboensis* by (1) MBSR 98–106 (vs. 131–140), (2) SMC 130–157 (vs. 183–195), (3) DTR 12–15 (vs. 9–10), (4) PP 6–8 (vs. 9), (5) LF1 7–10 (vs. 12–13), (6) LF4 9–12 (vs. 14–17), (7) LT1 7–9 (vs. 12–13), (8) IOS 24–28 (vs. 32–35), and (9) LT4 9–12 (vs. 14–15). Further-

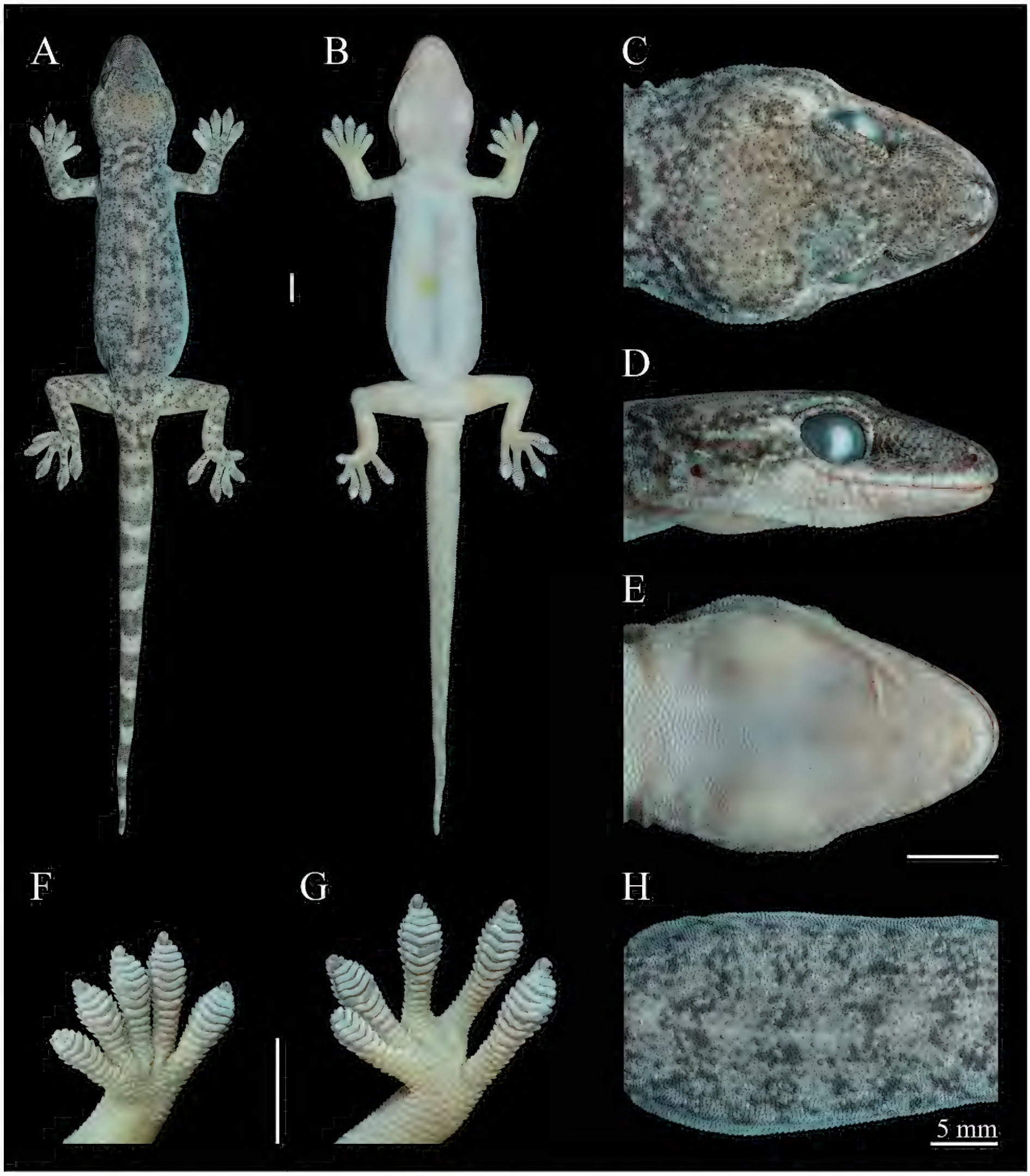

Figure 8. Preserved specimen of the female paratype of *Gekko tesselatus* sp. nov. (QHU R2025024). **A.** Dorsal view; **B.** Ventral view; **C.** dorsal view of head; **D.** Lateral view of head; **E.** Ventral view of head; **F.** Ventral view of hand; **G.** Ventral view of foot; **H.** Dorsal view of midbody. Photographs by YHX. Scale bars: 5 mm.

more, it can be distinguished from *G. paucituberculatus* by (1) MBSR 98–106 (vs. 136–142), (2) VS 31–39 (vs. 42–44), (3) SMC 130–157 (vs. 189–192), (4) DTR 12–15 (vs. 4), (5) PP 6–8 (vs. 12), and (6) IOS 24–28 (vs. 37).

The main characteristics that distinguish *Gekko tesselatus* sp. nov. from other species of the subgenus *Japonigekko* are summarized in Table 6. By having 6–8 precloacal pores in males, the new species can be easily distinguished from *G. aaronbaueri* Tri, Thai, Phimvohan, David & Teynié, 2015, *G. adleri* Nguyen, Wang, Yang, Lehmann, Le, Ziegler & Bonkowski, 2013, *G. canhi* canhi Rösler, Nguyen, Van Doan, Ho, Nguyen & Ziegler, 2010, *G. chinensis*, *G. jinjiangensis* Hou, Shi, Wang, Shu, Zheng, Qi, Liu, Jiang & Xie, 2021, *G. kaiyai* Zhang, Wu & Zhang, 2023, *G. khunkhamensis* Sithivong, Lo, Nguyen, Ngo, Khotpathoom, Le, Ziegler & Luu, 2021, *G. liui* Zhou, Zhou, Wang, Li, Zhang, Li, Shen, Liu & Rao, 2025, *G. melli*, *G. palmatus* Boulenger,

Figure 9. Habitat and field observations of *Gekko tesselatus* sp. nov. **A.** Macrohabitat of the new species in Se'ergu Town, Heishui County, Sichuan, China; **B.** Microhabitat of the new species; **C.** *Gekko tesselatus* sp. nov. in life, in situ; **D.** The sympatric *Lycodon multizonatus*. Photographs by YHX (**A–C**) and TXG (**D**).

1907, *G. prep*, *G. scabridus* Liu & Zhou, 1982, *G. scientiadventura* Rösler, Ziegler, Vu, Herrmann & Böhme, 2004, *G. sengchanthavongi* Luu, Calame, Nguyen, Le & Ziegler, 2015, *G. shibatai* Toda, Sengoku, Hikida & Ota, 2008, *G. similignum*, *G. tawaensis* Okada, 1956, *G. thakhekensis* Luu, Calame, Nguyen, Le, Bonkowski & Ziegler, 2014; *G. truongi* Phung & Ziegler, 2011; and *G. vertebralis* Toda, Sengoku, Hikida & Ota, 2008 (vs. 3–4 in *G. aaronbaueri*, 17–21 in *G. adleri*, 5 in *G. canhi*, 17–27 in *G. chinensis*, 4–5 in *G. jinjiangensis*, 9–12 in *G. kaiyai*, 0 in *G. khunkhamensis*, 20–23 in *G. liui*, 9–11 in *G. melli*, 23–30 in *G. palmatus*, 24 in *G. prep*, 10–15 in G. *scabridus*, 23–30 in *G. scientiadventura*, 4–5 in *G. sengchanthavongi*, 0–3 in *G. shibatai*, 17 in *G. similignum*, 0 in *G. tawaensis*, 1–5 in *G. thakhekensis*, 10–11 in *G. truongi*, and 0–1 in *G. vertebralis*).

By having MBSR 98–106, *Gekko tesselatus* sp. nov. can be distinguished from *G. bonkowskii* Luu, Calame, Nguyen, Le & Ziegler, 2015; *G. cib* Lyu, Lin, Ren, Jiang, Zhang, Qi & Wang, 2021; *G. hokouensis* Pope, 1928; *G. ichangensis* Cao, Sucharitakul, Tie, Suwannapoom, Yan & Chomdej, 2025; *G. japonicus* (Duméril & Bibron, 1836); *G. nadenensis* Luu, Nguyen, Le, Bonkowski & Ziegler, 2017; and *G. subpalmatus* (Günther, 1864) (vs. 117 in *G. bonkowskii*, 128–149 in *G. cib*, 119–130 in *G. hokouensis*, 127–145 in *G. ichangensis*, 130–144 in *G. japonicus*, and 129–156 in *G. nadenensis*).

By having DTR 12–15, *Gekko tesselatus* sp. nov. can be distinguished from *G. auriverrucosus* Zhou & Liu, 1982, *G. guishanicus* Lin & Yao, 2016, *G. swinhonis*, and *G. wenxianensis* Zhou & Wang, 2008 (vs. 16–20 in *G. auriverrucosus*, 0 in *G. guishanicus*, 6–8 in *G. swinhonis*, and 10 in *G. wenxianensis*).

Moreover, by having LT4 9–12, *Gekko tesselatus* sp. nov. can be distinguished from *G. alpinus* Ma, Shi, Shen, Chang & Jiang, 2024, *G. taibaiensis* Song, 1985, and *G. yakuensis* Matsui & Okada, 1968 (vs. 13–15 in *G. alpinus*, 7–8 in *G. taibaiensis*, and 15 in *G. yakuensis*).

Discussion

Molecular phylogenetic analyses recovered *Gekko tesselatus* sp. nov. as a strongly supported monophyletic lineage (SH = 100 / UFB = 100) within the subgenus *Japonigekko*. This lineage is nested within a well-supported clade (SH = 100 / UFB = 100) that also includes *G. fengshanensis*, *G. kwangsiensis*, *G. liboensis*, and *G. paucituberculatus*, together forming a distinct evolutionary assemblage. The close genetic relationships among

Table 5. Comparison of morphological characters among *Gekko tesselatus* sp. nov., *G. fengshanensis*, *G. kwangsiensis*, *G. liboensis*, and *G. paucituberculatus*; differences are shown in bold.

Species	*G. tesselatus* sp. nov.	*G. fengshanensis*	*G. kwangsiensis*	*G. liboensis*	*G. paucituberculatus*
	N = 14	**N = 6**	**N = 6**	**N = 2**	**N = 2**
SVLmax (mm)	65.3	79.9	69.7	79.7	85.9
NS	3 or 4	3	3	3	3
INS	0 or 1	0	0 or 1	0	0
SL	10 or 11	9–13	10–13	11	11
IL	9–12	10–13	11–13	9–11	9–10
IOS	22–26	22–27	**29–31**	**32–35**	**37**
PO	12–15	15–19	**18–20**	**17–18**	14–18
PM	2 (rarely 1)	2	2	2	2
GP	3–6	3–6	4–6	4–6	4–6
DTR	12–15	**9–11**	**9–11**	**9–10**	**4**
GSDT	7–9	9–10	8–10	9–10	8
SMC	130–157	**197–213**	**185–208**	**183–195**	**189–192**
MBSR	98–106	**149–161**	**143–156**	**131–140**	**136–142**
VS	31–39	**40–49**	**41–45**	38–41	**42–44**
LF1	7–10	**11–13**	10–13	**12–13**	10–11
LF4	9–12	12–16	12–14	**14–17**	12–13
LT1	7–9	**12–14**	**11–13**	**12–13**	**11**
LT4	9–12	**13–15**	**14–18**	**14–15**	**11–13**
PP	6–8	**9–12**	**9–10**	**9**	**12**
PAT	1 (rarely 2)	1	1	1	1
Web	Absent	**Present, weakly**	**Present, weakly**	**Present, weakly**	**Pesent, weakly**
Fore tubercles	Absent	Absent	Absent	Absent	Absent
Hind tubercles	Present	**Absent**	**Absent**	**Absent**	**Absent**
Tail tubercles	Present	**Absent**	Present	–	**Absent**
Sources	This study	Huang et al. (2025)	Yang et al. (2015)	Huang et al. (2025)	Wang et al. (2024)

these taxa suggest a potentially shared evolutionary origin. However, despite its phylogenetic affinity with the karst-dwelling species, *G. tesselatus* sp. nov. exhibits markedly different ecological and geographic characteristics. The new species inhabits highly weathered rocky slopes within hot–dry valleys of northwestern Sichuan Province, in contrast to its congeners, which are confined to warm limestone karst forests in southern China. These contrasting habitat preferences suggest that environmental heterogeneity has likely played a significant role in driving divergence within this clade.

Geographically, *Gekko tesselatus* sp. nov. is widely separated from its closest relatives. The nearest known rock-dwelling species, *G. liboensis*, occurs nearly 900 km away. It is therefore plausible that additional undescribed rock-dwelling species of *Japonigekko* exist in these underexplored areas. This observation underscores the need for more comprehensive and systematic fieldwork in southwestern and central China to improve our understanding of species diversity, distribution patterns, and evolutionary history within the subgenus *Japonigekko*.

The discovery of *Gekko tesselatus* sp. nov. raises the total number of species in the subgenus *Japonigekko* to 39, with 26 recorded from China, including seven species currently known from Sichuan Province: *Gekko tesselatus* sp. nov., *G. alpinus*, *G. chinensis* (record questionable), *G. cib*, *G. japonicus*, *G. jinjiangensis*, and *G. scabridus* (Cai et al. 2018; Hou et al. 2021; Lyu et al. 2021; Ma et al. 2024). With the exception of the newly described species, all of the above mentioned taxa exhibit varying degrees of adaptability to human-modified environments, such as buildings, bridges, or concrete embankments. In contrast, field observations indicate that *G. tesselatus* sp. nov. is almost never found within human settlements. Even at sites adjacent to villages or towns, individuals were only observed on nearby undeveloped rocky slopes, suggesting that the species may be more sensitive to human disturbance than its congeners. Given the current lack of data on population size, trends, and distribution range, we recommend that *Gekko tesselatus* sp. nov. be preliminarily classified as Data Deficient (DD) under the IUCN Red List criteria. Further field surveys in adjacent montane regions are essential to better understand its conservation status and to assess whether the species may qualify for listing under a threatened category in the future.

Table 6. Morphological characters of *Gekko* (*Japonigekko*); bold fonts indicate differences from the new species; Y = "Yes" or present, N = "No" or absent; differences are shown in bold for clarity.

No.	Species	SVLmax	SL	IL	IOS	DTR	SMC	MBSR	VS	LT1	LT4	Web	Fore tubercles	Hind tubercles	Tail tubercles	PP
1	*G. tesselatus* sp. nov.	65.3	10 or 11	9–12	22–26	12–15	130–157	98–106	31–39	7–9	9–12	N	N	Y	Y	6–8
2	*G. aaronbaueri*	80	**13–14**	10–11	**34–37**	0	–	98–104	39–43	**14–17**	**14–16**	**Y**	N	**N**	**N**	**3–4**
3	*G. adleri*	75.3	10–15	9–13	**27–36**	7–11	**168–190**	**123–144**	35–44	**11–14**	11–15	**Y**	N	Y	Y	**17–21**
4	*G. alpinus*	74.16	9–13	8–10	22–28	12–17	**158–18**9	92–114	32–39	8–11	**13–15**	N	**Y**	Y	Y	**4–7**
5	*G. auriverrucosus*	69	9–11	9–11	26–27	**16–2**0	–	–	–	6–8	6–8	N	**Y**	Y	Y	8–11
6	*G. bonkowskii*	69.2	**12–14**	10–11	**49–50**	**0**	154–169	**117**	37–40	**11–13**	**15**	**Y**	N	**N**	**N**	6
7	*G. canhi*	99.2	**14**	10–12	**49–50**	11–12	**168–170**	**205–227**	**49–51**	**13–16**	**14–17**	N	N	Y	**N**	5
8	*G. chinensis*	72	10–14	9–13	**35–48**	**10**	156–167	**118–140**	37–39	8–10	9–12	**Y**	N	Y	Y	**17–27**
9	*G. cib*	66.4	10–12	10–14	**28–36**	**0**	**171–196**	**128–14**9	37–45	9–13	9–17	**Y**	N	**N**	**N**	7–9
10	*G. fengshanensis*	79.9	9–13	10–13	22–27	**9–11**	**197–213**	**149–161**	**40–49**	**12–14**	**13–15**	**Y**	N	**N**	**N**	**9–12**
11	*G. guishanicus*	64	–	–	–	**0**	–	–	–	8–10	8–10	**Y**	N	**N**	**N**	6–8
12	*G. hokouensis*	70	10–14	8–11	**30–33**	12–18	153–174	**119–130**	36–43	8–11	**15–18**	N	N	**N**	Y	5–9
13	*G. ichangensis*	66.5	7–11	7–11	**27–36**	10–12	**174–195**	**127–145**	39–47	**12–15**	**13–18**	**Y**	**Y**	Y	Y	5–8
14	*G. japonicus*	74	9–13	8–13	**32–35**	9–14	**169–188**	**130–144**	39–44	**10–12**	**14–16**	N	**Y**	Y	Y	4–9
15	*G. jinjiangensis*	61.6	7–10	6–9	20–24	12–16	146–169	**111–149**	31–47	8–11	11–15	N	**Y**	Y	Y	**4–5**
16	*G. kaiyai*	64.99	9–12	9–13	22–33	11–18	157–209	99–121	30–43	8–9	7–11	N	**Y**	Y	Y	**9–12**
17	*G. khunkhamensis*	75.2	9–10	9–10	**31–32**	**0**	**181–185**	**127–138**	**42–45**	**13–14**	**14–15**	**Y**	N	**N**	**N**	**0**
18	*G. kwangsiensis*	69.7	10–12	11–13	**29–31**	**9–11**	**185–208**	**143–156**	**41–45**	**11–13**	**13–18**	**Y**	N	**N**	Y	**9–11**
19	*G. liboensis*	79.7	11	9–11	**32–35**	**9–10**	**183–195**	**131–140**	38–41	**12–13**	**14–15**	**Y**	N	**N**	–	**9**
20	*G. liui*	56.67	11–13	11–12	**37–42**	**7–8**	**140–148**	**103–118**	34–39	**10–11**	12–13	**Y**	N	**N**	Y	**20–23**
21	*G. melli*	80.3	10–13	9–12	**34–40**	**0**	**171–192**	**148–160**	**44–46**	**10–12**	11–14	**Y**	N	**N**	**N**	**9–11**
22	*G. nadenensis*	77.1	**12–14**	10–12	**28–30**	**0**	**175–185**	**123–140**	38–40	**13–15**	**14–16**	**Y**	N	**N**	**N**	6
23	*G. palmatus*	79.7	11–15	9–13	**27–36**	4–12	**160–191**	**116–147**	36–47	**10–13**	10–16	**Y**	N	**N**	Y	**23–30**
24	*G. paucituberculatus*	85.9	11	9–10	**37**	**4**	**189–192**	**136–140**	**42–44**	**11**	11–13	**Y**	N	**N**	**N**	**12**
25	*G. prep*	75.7	**14**	11	**37–38**	12	**144–152**	**122–126**	38–40	**11–12**	12–13	**Y**	N	**N**	Y	**24**
26	*G. scientiadventura*	73	**12–14**	9–13	**41–51**	**0**	**118–140**	**139–143**	38–48	**12–15**	**14–17**	**Y**	N	**N**	Y	**23–30**
27	*G. scabridus*	64	9–11	9–11	**30**	**17–21**	–	–	–	6–9	7–9	N	**Y**	Y	Y	**10–15**
28	*G. sengchanthavongi*	77.3	8–10	6–7	**28–32**	**0**	**175–184**	**120–135**	35–43	**11–14**	13–17	**Y**	N	**N**	**N**	**4–5**
29	*G. shibatai*	70.9	10–13	10–14	**37–52**	5–14	–	**114–134**	–	**11 or 12**	9–16	N	N	**N**	Y	**0–3**
30	*G. similignum*	58.9	**12–14**	11	**46–48**	**11**	–	**144–153**	–	**11–13**	12–14	**Y**	N	**N**	Y	**17**
31	*G. subpalmatus*	65.8	8–12	7–12	**28–37**	**0**	144–190	**129–15**6	39–46	9–12	11–14	**Y**	N	**N**	**N**	5–9
32	*G. swinhonis*	66	7–12	7–11	23–24	**6–**8	–	–	**40**	6–9	6–9	N	**Y**	Y	–	7–9
33	*G. taibaiensis*	69	9–10	8–10	**28**	–	–	–	–	6–7	**7–8**	**Y**	–	–	–	4–6
34	*G. tawaensis*	71	15	**13**	–	**0**	–	–	–	**10**	12	N	N	**N**	**N**	**0**
35	*G. thakhekensis*	79.2	**12–14**	10–11	22–26	**0**	**165–174**	**110–116**	32–40	**11–13**	**14–15**	**Y**	N	**N**	**N**	**1–5**
36	*G. truongi*	95.9	**13–15**	11–13	**45–48**	**0**	**160–172**	**131–143**	35–36	**11–13**	**15–17**	N	N	**N**	**N**	**10–11**
37	*G. vertebralis*	69.2	10–15	10–15	**35–50**	2–12	–	**112–139**	**10–12**	–	9–17	N	N	**N**	**N**	**0–1**
38	*G. wenxianensis*	59	**12**	11	–	**10**	–	–	**42–44**	6	9	N	N	Y	–	6–8
39	*G. yakuensis*	72	**12–13**	9–13	–	–	–	–	–	**10**	**15**	N	N	**N**	Y	6–8

Figure 10. Comparison of *Gekko tesselatus* sp. nov. and four closely related species in life, in situ. **A.** *Gekko tesselatus* sp. nov., unvouchered adult male individual from Se'ergu, Heishui, Sichuan, China; **B.** *Gekko tesselatus* sp. nov., unvouchered juvenile individual from Se'ergu, Heishui, Sichuan, China; **C.** *G. liboensis*, unvouchered individual from Libo, Guizhou, China; **D.** *G. fengshanensis*, NHMG 202408007, adult male from Fengshan, Guangxi, China; **E.** *G. kwangsiensis*, unvouchered adult female individual from Nanning, Guangxi, China; **F.** *G. paucituberculatus*, unvouchered individual from Baise, Guangxi, China. Photographs by YHX (**A, B**), Dan-Yang Zhou (**C, F**), reproduced from Huang et al. (2025) (**D**), and Yang (2015) (**E**).

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